

OIPE

RAW SEQUENCE LISTING

DATE: 10/24/2002

PATENT APPLICATION: US/10/057,487 TIME: 16:24:03

Input Set : A:\87020073.txt

Output Set: N:\CRF4\10242002\J057487.raw

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3 <110> APPLICANT: Wyeth
     5 <120> TITLE OF INVENTION: Aggrecanase Molecules
     7 <130> FILE REFERENCE: 08702.0073
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/057,487
C--> 9 <141> CURRENT FILING DATE: 2002-01-25
     9 :150: PRIOR APPLICATION NUMBER: 60/241,469
     10 -:1515 PRIOR FILING DATE: 2000-10-18
     12 <160 NUMBER OF SEQ ID NOS: 8
     14 -: 170: SOFTWARE: PatentIn version 3.1
     16 + 210 \times SEQ ID NO: 1
     17 <211> LENGTH: 242
     18 -: 212> TYPE: PRT
     19 <213> ORGANISM: Homo sapiens
     21 <400> SEQUENCE: 1
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     31 Gln Arg Gln Arg Gln Arg Gln Arg Ala Ala Gly Gly Ile Leu His
                                    40
     35 Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His Gln
                                55
     39 Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala Glu
                                                75
                           70
     43 Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu Val
                        85
                                            90
     47 Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala
                                        105
                    100
     51 Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr Ile
                                    120
     55 Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu Tyr
                                                   140
                               135
     59 Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val Arg
                                               155
                           150
     60 145
     63 Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys Leu
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                        165
     67 Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His Glu
                                        185
                    180
     68
     71 Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser Gly
                                    200
     72 195
     75 Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro Arg
                                215
     79 Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser Leu
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00 223			
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95 gotgaatgog gagtggggac g	gacgtccgg agggetgget g	gaagetege gegeeeetee	120
97 cacgaggegg gegetaeetg a	graggetea gragetgreg q	cqqctgcag ggggaccagg	180
an chaddacade acadadeded a	caccatica aagccatcac g	tgtccgctg gggccgcagc	240
101 agataccada cacaccatea	tactocagge egaagetgtg	cccaatctca tygycaatgg	3(11)
103 tgactcccag gtcgaagcca	gtgtcctcgg taatgaggca	gctccaggtt ggggagcagg	360
105 caccgcccag ctqqqtqacq	coccecacet geogettace	atcaggcaac tccaggtcaa	420
107 acctantinat atagaggacc	aggtcagcat ggccaggatc	egiglegied leagggerga	480
100 tagtetaget ceacceacag	acgctcagca gggacgaggt	gaggingger graduating	540
111 gagcaccete aggetetgte	agaatgacca tottcaccag	gtgcacccga aactgagccc	δ (10
113 ccanddaedd afecedaage	agttctgccc cgatgttgag	gilggigage acatagegee	640
115 etatateate etaataaace	tagaagacat cqqqqcccac	ggccaccage ageteeagge	720
117 ataggatace acctagagee	cacctctacc tctacctcta	cciciggaay ccayyyyaay	780
110 garagegaee ttttaagaga	gcaccagggc tcaagtaaga	agacacygee cycygeeee	840
1 11 paggotgaag acaactcggg	tactacacac acageggeee	Cocaglicoc Liceggegee	900
1 12 aggregation at coccation	cagatettag agaggteete	ddGffdGGG agreadacte	960
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138 tacgactcac tatagggaga	acctcgagtt tgactggggc	aagccgagga coloccaag	120
110 atcommate gogatgagag	atgcgaacgc cggaagggaa	Ciggggggcc gergracaca	180 240
140 taggacccga gttgtcttca	ggctttggag ccacaggccg	tgtcttctta cilgagood	300
111 gatactccct taaaaggccg	coctecttee ectagetice	agaggcagag gcagaggcag	360
116 aggragacta cagacagcat	cctacacctg gagetgetgg	Lggccglggg ccccgatgtc	420
110 trecaggete accaggagga	cacagagege tatgtgetea	Ccaaccicaa catcyyyycu	420
150 gaagtgette gggacccgte	cctagagact cagtttcggg	Lgcacciggi gaagaiggic	540
150 attotoacad adoctoaddd	toctccaaat atcacagcca	accedacete greecegery	600
15.1 accentetata agtagageca	gaccatcaac cctgaggacg	acacggatee tygecatyet	б ф О
15/ magatagtag tatatataga	taggtttgac ctggagttgc	Cidalidara condendade	720
158 cygygcgtca cccagctggg	cggtgcctgc tccccaacct	ggagetgeet cattacegag	780
160 and taget togacetage	antraccatt decealdada	Liqqqdacag Circggcccg	840
160 *** and and acadeaccean	cadeddetae ddeeccaded	gacacqugat ggcttcggac	900
161 gragecacae cecacaecaa	cotogootaa tooccouyca	quegetygea getgetgage	960
166 atactopaat aacacccacc	-ccataggagg ggcgcgcgag	Cilcoagoda godocedaga	1020
168 egteegteec cacteegeat	teagecetee treetgreet	acceptedat congacoucu	1045
170 ctogtaggee tetttggeeg	aattc		
173 <210> SEQ ID NO: 4			

RAW SEQUENCE LISTING

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Input Set : A:\87020073.txt

Output Set: N:\CRF4\10242002\J057487.raw

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181 gatggetteg gaacggegee geeeegegee ggeetegeet ggteeeetg cageegeegg
                                                                          120
183 magetgetga geetgeteag acceptecet eegtegeege teeetetget ggeeaeceae
                                                                          180
185 ctctgcgccg gcaggagcct tagtcttggt cccagccaag agccggctcc tggtggggg
                                                                          240
187 egegggeega gaacteetgt teccacteae aaaaggeeae gettecaaae gettecatee
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189 togtgeccae tecteogtee egectectee eggtgtacae eeegggaetg ageegggeet
                                                                          360
191 gageegggee ttgtegeage geatgaeggg egegetggtg tgggaeeege egeggeetea
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193 accegggtee geggggeace egeggaatge geacetggge etetaetaea gegecaacga
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145 geagtgeege gtggeetteg geeceaagge tgtegeetge acettegeea gggageaeet
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197 ggtgagtetg eeggeggtgg eetgggattg getgtgaggt eeeteegeat caeceagete
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199 acqtccccc aaacqtgcat ggatatgtgc caggccctct cctgccacac agacccgctg
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201 gaccaaagca getgeageeg ecteetegtt ceteteetgg atgggacaga atgtggegtg
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203 gagaagtggt getecaaggg tegetgeege teeetggtgg agetgaeeee catageagea
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205 gtgcatggge getggtctag etggggtccc egaagtcett geteeegete etgeggagga
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207 ggtgtggtca ccaggaggcg gcagtgcaac aaccccagac ctgcctttgg ggggcgtgca
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209 tgtqttggtg etgaeeteca ggeegagatg tgeaacaete aggeetgega gaagaeeeag
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211 ctgqagttca tgtcgcaaca gtgcgccagg accgacggcc agccgctgcg ctcctcccct
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\pm 13 ggeggegeet cettetacea etggggtget getgtaceae acageeaagg ggatgetetg
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215 tycagacaca tytyccygyc cattygcyay agettcatca tyaagcytyg agacagette
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217 ctcyatggga cccggtgtat gccaagtggc ccccgggagg acgggaccct gagcctgtgt
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219 gtgtcgggca gctgcaggac atttggctgt gatggtagga tggactccca gcaggtatgg
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221 gacaggtgcc aggtgtgtgg tggggacaac agcacgtgca gcccacggaa gggctctttc
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223 acagetggca gagegagaga atatgteacg tttetgacag ttacceccaa eetgaceagt
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225 gtctacattg ccaaccacag gcctctcttc acacacttgg cggtgaggat cggagggcgc
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227 tatgtcgtgg ctgggaagat gagcatetee cetaacacca cetacceete ecteetggag
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 229 gatggtcgtg tcgagtacag agtggccctc accgaggacc ggctgccccg cctggaggag
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 233 cagoteatge acateagetg gtggageagg cotggeettg gagaacgaga cotgtgtgee
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 239 cacctetgea ggggagaagg eteceteece atggggeage ateaggaegg gggeteaage
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 243 ggagetgegt tteetgtgea tggaetetge ceteagggtg eetgteeagg aagagetgtg
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 245 taggeotagea ageaageetg ggageeggeg ggaggtetge caggetgtee egtgeeetge
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 247 toggtggcag tacaagetgg eggeetgeag egtgagetgt gggagagggg tegtgeggag
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 249 gatectgtat tgtgcccggg cccatgggga ggacgatggt gaggagatec tgttggacac
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 255 <211> LENGTH: 365
 256 <212> TYPE: PRT
 257 <213> ORGANISM: homo sapiens
 259 <220> FEATURE:
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264 <220> FEATURE:

260 <221> NAME/KEY: MISC_FEATURE

261 <223> OTHER INFORMATION: unknown amino acid

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265 <221> NAME/KEY: MISC_FEATURE 266 <222 LOCATION: (365)..(365) 267 < 223 OTHER INFORMATION: unknown amino acid 270 <4005 SEQUENCE: 5 272 Met Asp Met Cys Gln Ala Leu Ser Cys His Thr Asp Pro Leu Asp Gln 276 Ser Ser Cys Ser Arg Leu Leu Val Pro Leu Leu Asp Gly Thr Glu Cys 20 277 280 Gly Val Glu Lys Trp Cys Ser Lys Gly Arg Cys Arg Ser Leu Val Glu 40 35 184 Leu Thr Pro Ile Ala Ala Val His Gly Arg Trp Ser Ser Trp Gly Pro 55 188 Arg Ser Pro Cys Ser Arg Ser Cys Gly Gly Gly Val Val Thr Arg Arg 75 70 191 Arg Gln Cys Asn Asn Pro Arg Pro Ala Phe Gly Gly Arg Ala Cys Val 85 90 296 Gly Ala Asp Leu Gln Ala Glu Met Cys Asn Thr Gln Ala Cys Glu Lys 105 100 300 Thr Gln Leu Glu Phe Met Ser Gln Gln Cys Ala Arg Thr Asp Gly Gln 120 115 304 Pro Leu Arg Ser Ser Pro Gly Gly Ala Ser Phe Tyr His Trp Gly Ala 135 140 305 130 308 Ala Val Pro His Ser Gln Gly Asp Ala Leu Cys Arg His Met Cys Arg 155 150 312 Ala Ile Gly Glu Ser Phe Ile Met Lys Arg Gly Asp Ser Phe Leu Asp 170 165 316 Gly Thr Arg Cys Met Pro Ser Gly Pro Arg Glu Asp Gly Thr Leu Ser 180 185 320 Leu Cys Val Ser Gly Ser Cys Arg Thr Phe Gly Cys Asp Gly Arg Met 200 324 Asp Ser Gln Gln Val Trp Asp Arg Cys Gln Val Cys Gly Gly Asp Asn 215 210 328 Ser Thr Cys Ser Pro Arg Lys Gly Ser Phe Thr Ala Gly Arg Ala Arg 235 230 329 225 332 Glu Tyr Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr 250 245 336 Ile Ala Asn His Arg Pro Leu Phe Thr His Leu Ala Val Arg Ile Gly 265 337 260 340 Gly Arg Tyr Val Val Ala Gly Lys Met Ser Ile Ser Pro Asn Thr Thr 275 280 344 Tyr Pro Ser Leu Leu Glu Asp Gly Arg Val Glu Tyr Arg Val Ala Leu 295 348 Thr Glu Asp Arg Leu Pro Arg Leu Glu Glu Ile Arg Ile Trp Gly Pro 315 310 352 Leu Gln Glu Asp Ala Asp Ile Gln Val Gly Gly Val Arg Ala Gln Leu 325 330 356 Met His Ile Ser Trp Trp Ser Arg Pro Gly Leu Gly Glu Arg Asp Leu 345 340 W--> 360 Cys Ala Arg Gly Arg Trp Pro Gly Gly Ser Ser Asp Xaa

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- 360 355 364 <:210> SEQ ID NO: 6 365 <211> LENGTH: 738 366 -: 212> TYPE: PRT 367 (213> ORGANISM: homo sapien 369 -(220> FEATURE: 370 - 221> NAME/KEY: MISC_FEATURE 371 <222> LOCATION: (43)..(43) 372 <223> OTHER INFORMATION: unknown amino acid 375 <220> FEATURE: 376 <201> NAME/KEY: MISC_FEATURE 377 <222> LOCATION: (192)..(192) 378 <223> OTHER INFORMATION: unknown amino acid 381 <220> FEATURE: 382 <221> NAME/KEY: MISC_FEATURE 383 <222> LOCATION: (255)..(255) 384 <223 > OTHER INFORMATION: unknown amino acid 387 -: 220 > FEATURE: 388 - 1221 > NAME/KEY: MISC_FEATURE 389 +222> LOCATION: (258)..(258) 390 <223> OTHER INFORMATION: unknown amino acid 393 <220> FEATURE: 394 <221> NAME/KEY: MISC_FEATURE 395 <222> LOCATION: (374)..(374) 396 <223> OTHER INFORMATION: unknown amino acid 399 <220> FEATURE: 400 <221> NAME/KEY: MISC_FEATURE 401 <222> LOCATION: (397)..(397) 402 <223> OTHER INFORMATION: unknown amino acid 405 <220> FEATURE: 406 <221> NAME/KEY: MISC_FEATURE 407 <222> LOCATION: (452)..(452) 408 <223> OTHER INFORMATION: unknown amino acid 411 <220> FEATURE: 412 <221> NAME/KEY: MISC_FEATURE 413 <222> LOCATION: (458)..(458) 414 <223> OTHER INFORMATION: unknown amino acid 417 <220> FEATURE: 418 <221> NAME/KEY: MISC_FEATURE 419 <222> LOCATION: (475)..(475)

- 420 <223> OTHER INFORMATION: unknown amino acid
- 423 <220> FEATURE:
- 424 <221> NAME/KEY: MISC_FEATURE
- 425 <222> LOCATION: (487)..(487)
- 426 <223> OTHER INFORMATION: unknown amino acid
- 429 (400> SEQUENCE: 6
- 431 Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser Gly Cys Gly Pro
- 432 1
- 435 Ser Gly His Val Met Ala Ser Glu Arg Arg Pro Ala Pro Ala Ser

RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 10/24/2002 TIME: 16:24:04

PATENT APPLICATION: US/10/057,487

Input Set : A:\87020073.txt

Output Set: N:\CRF4\10242002\J057487.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 365

Seq#:6; Xaa Pos. 43,192,255,258,374,397,452,458,475,487

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/057,487 TIME: 16:24:04

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Input Set : A:\87020073.txt

Output Set: N:\CRF4\10242002\J057487.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:360 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:352 L:439 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:32 L:475 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:176 L:491 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:240 L:495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:256 L:523 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:368 L:527 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:384 L:543 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:448 L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:448 L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:464 L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:480